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| OM nucleic - nu                       | nucleic search, using sw                                  | model   |  |
|---------------------------------------|---|---|--|
| Run on:                               | =   | :26:23 ; Search time 7464 Seconds (without alignments) 10994.736 Million cell updates/sec |  |
| Title:<br>Perfect score:<br>Sequence: | US-09-701-572-1<br>2006<br>1 gattcggcacgaggaagaaa         | аддаааааааааааааааа 2006  |  |
| Scoring table:                        | IDENTITY NUC<br>Gapop 10.0 , Gapext 1                     | 1.0   |  |
| Searched:                             | 2888711 segs, 20454813386                                 | 3386 residues   |  |
| Total number of                       | f hits satisfying chosen parameters                       | n parameters: 5777422   |  |
| Minimum DB seq<br>Maximum DB seq      | length: 0<br>length: 200000000                            |   |  |
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| Color  | Description | 8931 Sec<br>9404 Med | AY099585 Arabidop | 35    | 35 Medic | BT002165 Arabidops<br>AY099581 Arabidops | 37 Xenop | Xenopus<br>38 Danio | 616 Mus | 809 Mus<br>62 Homo | 15 Ношо вар | BT008152 Synthetic<br>BC013413 Homo sapi | 10 Ношо вар | 168 Homo sap<br>103 Drosophi | 46 Gallus g | y/ Homo sap<br>Drosophila | 4   | 95 Sequences | 75 S.pombe | ωū  | 73 Ustilag | 21 Schizos | Schizosac | Schizosac   | 09 Seguence | 865 Drogophi<br>715 Drogophi | 31 Drosophi | 75 Spisula | 29 Drosophi | 42 Drosophi | 118 Dr | ez prosopni |           | linear PAT 06-SEP-2000 |            |         |         | ), Embryophyta; Tracheophyta;<br>ledons; core eudicots;<br>Papilionoideae; Trifolieae; | •                  |
|--|-------------|----------------------|-------------------|-------|----------|--|----------|---------------------|---------|--------------------|-------------|--|-------------|------------------------------|-------------|---------------------------|-----|--------------|------------|-----|------------|------------|-----------|-------------|-------------|------------------------------|-------------|------------|-------------|-------------|--------|-------------|-----------|------------------------|------------|---------|---------|--|--------------------|
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LVSTHGYSGNQITUTWRYPTMSKLATLTGHTYRVLYLAISPDGGTIVTGAGDETLRFWN

VPPSFRSQNTESEIGALGARTTIR"

3 398 C 441 g 612 t
  Plant protein with repeated wd40 motifs, nucleic acid coding for said protein, and uses thereof
Patent: WO 9964451-A 1 16-DEC-1999;
CEBOLLA ANGEL (FR); KONDOROSI EVA (FR); KONDOROSI ADAM (FR); CENTRE NAT RECH SCIENT (FR)
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                          99.0%; Score 1986.4;
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Spermatophyta; Magnoliophyta; endicotyledons; Core endicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

I (bases I to 1988)
Cebolla,A., Kondorosi,A. and Kondorosi,E.
A plant cell gcle regulator that controls endoreduplication and cell differentiation
Unpublished
Cebolla,A., Kondorosi,A. and Kondorosi,E.
Cebolla,A., Kondorosi,A. and Kondorosi,E.
Direct Submission
L Submitted (21-UUL-1998) ISSY, CNRS, Avenue de la Terrasse, Bat. 23, 100 and 100
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mRNA, complete cds.
AP079404.1 GI:4558461
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protein (At4g22910)

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Arabidopsis thaliana putative fizzy-related
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I (bases 1 to 1541)
SS Trippy, M., Southwick, A., Karlin-Neumann, G., Rayben, M., Miranda, M., Palm, C., U., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Kawai, J., Kim, C., Lin, J., Lin, S. X., Ishida, J., Kamiya, A., Kamiya, A., Kamin, J., Kawai, T., Sakuraai, T., Sakura
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to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as Pis.
Location/Qualifiers
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/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                             Query Match
Best Local Similarity
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| 1377   ACTCCCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCAAAGCTGGCGACTCTTA   1436   | AY099585  N Arabidopsis thaliana putative fizzy-related protein (At4922910) AY099585 AY099585.1 GI:20466238 FLI CONA. Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) | Spermatophyra; Magnoliophyra; eudicotyledons; core everogids; eurosids II; Brassicales; Brassicaceae; Arabi I (bases I to 1865)  Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Nelm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kam, Kawai, J., Kim, C., Lin, J., Liu, S.K., Narusaka, M., Phan Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Shinn, P., Shinn, P., Shinn, P., Theologis, A. and Davis, R.W. | Direct Submission Submitted (24-APR-2002) DNA Sequencing and Technology Center, Submitted (24-APR-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA e-mail for correspondence: arab@sequence.stanford.edu RIKEN Genomic Sciences Center (GSC) members carried out the | Ocitedion and citeties of Arthurs, National, 15hida,J., Arabidopsis Full-Length Conformal, F., Carninci, P., Kawai,J., Sakurai,T., Carninci,P., Kawai,J., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPI coPNAs: Nguyen,M., Salun,C.J., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Sower,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., M., Chang,M.K., M., Chang,M.K | Nguyen, M, (SSP/Stanf,<br>equally to this work<br>(SSP/Stanford) conti<br>1.1865  <br>/organism="//mol_type="r//mol_type= | /clone="RAPL09-63-A14 (R24687)"<br>/note="This clone is in pBluescript<br>ectype: Columbia"<br>1. 1865<br>/gene="At4922910"<br>/note="synonym: F7H19.90"  |
|--|--|--|--|--|--|---|
| 8 6 8 6 8 6 8 6  | RESULT 4 AC1099585 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM   | REFERENCE<br>AUTHORS   | TITLE<br>JOURNAL<br>COMMENT  |  | FEATURES<br>BOURC  | gene  |
| 158   CONSERVATIVE   0, Mismatches   312; Indels   27; Gaps   4;   365   306   CCTCACCTTCTCGAACATCTACTCCGATAGATCTACTCGAACATCTACTCGAACATCTACTCGAACATCTACTCGAACATCTACTCGAACATCACTTCGAACATCACTTCGAACATCAACTCTACTCGAACATCCAACATCAACTCCAACATCAACTCCAACATCAACTCCAACATCAACATCCAACATCCAACATCCAACATCCAACATCCAACATCCAACATCCAACATCGAACATCCAACATCCAACATCCAACATCCAACATCCAACATCTCCTC |  | 500 TATTGGATGCACCGGCCTTGCAAGATGATTTTTATCTGAALCTTGTGAATGGTCTGCAC 559  717 ACAATGTGTTGGCTGTTGGTAACTGTGTCTCTTGTAATGCTTGTAGCAGCA 776   | 837 AACGTGGTACTCATGCTGTTGGAACTAACAATGGTAAAGTTCAGATTTGGGATGCAG 896  [   |  | 920 AGIGGTCTTATGACAACAGAGAGCTAGCATCGGTGGAACGACAATAGGCTTTTTGTAT 979  1137 GGAATCAACCTCAACCTGTCTCTCAAGTACTGTGAGCACAGCAGCTGTTAAAG 1196  980 GGAACCAACTTCAACACAGTTTTGAATATAGTGAACACATGCTGTTAAAG 1039  1197 CTATTGCATCGTCCTCCTCATCATAGTAATATAGTGAACACAGAGAACTGCAGATA 1256  1197 CTATTGCATGGTCTCCTCATCATAGACTTCTCCATCTGGAGGAGACTGCAGATA 1256  1040 CCATTGCTTGGTCTCCTCATGTTCATGGGCTTCTTCTCTTTCTCTTTGTTGTTGTTGTTGTTGTT   | 1257 GATGTATTCGTTTTTGGAATACCACCACAAACTCACCCCTTAGCTGTATGGACACTGGAA 1316 1100 GATGCATATTGGAATACAACCACGAATACTCATTTAAGTTCCATAGATACTTGCA 1159 1317 GTCAGGTTTGCAATCTTGCTCTGGTCCAAAATGTCAACGAACTAGTAGACACACATGGGT 1376 1317 GTCAGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAACTAGTAAGAACACACATGGGT 1376 1160 GTCAGGTATGCAATCTTGGTCTAAAAATGTCAAAGAACTATAGCACACACA |

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Fil CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiphantae; Streptophyta; Core endicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 1459)
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1077 AGTGGTCATATGATAACCGTGAGTTGGCATCTGGAGGAAATGACAACAAATTGTTTT 1136
                                                                                           986 AGTGGTCTTATGACAACAGAGCTAGCATCTGGTGGAAACGACAATAGGCTTTTTTGTAT 1045
                                                                                                                                                                                      1137 GGAATCAACACTCAACCCAGCCTGTCCTCAAGTACTGTGAGCACACAGCAGCTGTTAAAG 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATTGCTTGGTCTCCTCATGTTCATGGGCTTCTTGCTTCTGGTGGTGGTACTGCTGATA 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1257 GATGTATTCGTTTTTGGAATACAACCACAAACTCACACCTTAGCTGTATGGACACTGGAA 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1226 GTCAGGTATGCAATCTAGCTTGGTCTAAGAACGTAAACGAGCTTGTTAGCACACACGGAT 1285
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                                                                           /product="putative fizzy-related protein"
/protein id="AAM20437.1"
/brotein id="AAM20437.1"
/db xref="col:2046627.1"
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/db xref="col:2046627.1"
/translation="www.meredpranultnesserning-pammypvvslbranultna-
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PGPSTPERKDITGPSSSNIYBFRYTETHRSLNSSPPRGVDDDSPGVSRFRYD-
PRSPYKKLDAPALODPFYLNIVDWSAQNYLAVGLGNCVTMWAGSSKYTKLCDGAED
SVCSVGWALRGTHLAVGTSTGKVQIWDASRCKRTRTWEGHRLRVGALAWGSSVLSGS
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VLKYSEHTAAVKALAMSPHYHGLLASGGGTAARCIRFMYTTWTHLSIDTCSGVCNL
AWSKNVNELVSTHGYSGNIJVWKFYPTMSKIATLIGHTYRVLYLAVSPDGQTIVTGAG
DETLARWNVFDSRSQNTDSELGSSFFCRTTIR"
374 c 393 g 554 t
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Location/Qualifiers
    The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J. Satcou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                    Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUMI (ORF) clones using the RAFL cDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, G.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Meuk, R., Jans, M., Naywen, M
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Pred. No. 2.6e-155;
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1911)

S Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M.K.,

Goldsmith, A. D., Lee, J. M., Quach, H. L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Karlin, Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Bavis, R. W., Ecker, J. R. and Theologis, A., Shinozaki, K.,

Arabidopsis Pull Length cDNA Clones

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yearda, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yu, G., Yu, S., Boweri, L., Carninoi, P., Chen, H., Chen, H., Chen, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Salou, M., Seki, M., Shin, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Direct Submission

L. Submitted (19-NOV-2011) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA 'RIKEN Arabidopsis Pull-Length CDNA): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Ramiya, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                           Arabidopsis thaliana putative Srwl protein (At4g11920) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDRAs: Yamada,K., Banh,J., Chang,B., Dale,J.M., Goldsmith,A.D., Lee,J.M., Chang,B., Dale,J.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Mitanda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.
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1. .1911
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AY063875.1 GI:17380837
       1415 CAACAATCCGGTGA 1428
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VERSION
KEYWORDS
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ORGANISM
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JOURNAL
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AUTHORS
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JOURNAL
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LVFRSFRGYSQNQIIVWRXPTRKKLATITGHTYRVLYLAISPDGGTIVTGAGDETLRFWN
VFPSFRGYQNTESEIGALSLGRTIR"
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5572. .S634,5735. .5929,6459. .6560,6651. .6713,6827.
7452. .>7505)
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Pred. No. 1.3e-125;
0; Mismatches 37;
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<2461. .>7505
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Gif Sur Yvette 91198, France
Location/Qualifiers
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Best Local Similarity 84.9%;
Matches 738; Conservative 0
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gene, complete cds.
AF134835.1 GI:7158291
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Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Spermatophyta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Trifolieae;
                                                          880 TAAGAGTIGGAGCCTIGGCAIGGAGCICATCTGTICTICTACTCAGGTAGTAGAGACAAGA 939
                                                                                                                                                  940 GCATACTTCAGAGAGACATTCGTACTCAAGAAGATCATGTCAGTAAACTTAAAGGTCACA 999
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1 (bases 1 to 8450)
2 (cebolla, A., Vinardell, J.M., Olah, B., Kiss, E., Roudier, F.,
Kondorosi, A. and Kondorosi, E.
The mitotic inhibitor ccs52 is required for endoreduplication and
polyploidy-dependent cell enlargement in plants
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Vinardell, J.M. and Kondorosi, E.
Direct Submission
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Arabidopsis thaliana cell cycle switch protein (At5g13840) mRNA,
2774 CGCCGTCGATGACATTGCCGAATAGGAATATTTTTAGGTATAAGACGGAGACGAGACAGT 2833
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                        2834 CCATGCACTCGCTTTCGCCGTTTATGGATGATGATTTTGTTCCTGGTATTAATCATAGTC
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                                                                                          CCATGCACTCGCTTTTCGCCGTTTATGGATGATTTTTGTTCCTGGTGTTAATCATAGTC
                                                                                                                                                                                                                                                    e-mail for correspondence: arab@sequence.stanford.edu
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/translation="maspostktglnlpagmnotslrletrssfrgisslspskxt CSDRFIPCRSSSRLHARDLODKEPTTPVKEGGNEAYSRLLKSELRGSDFASPLLSPAG GQGSASSPMSPCTNMLRFKTDRSNSSPSSPFSPSILGNDNGHSSDSSPPPKPPK

product="cell cycle switch protein" protein id="AAN72176.1" db xref="d1:25084105"

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/note="This clone is in pENTR/SD-dTopo This is a cloned PCR product using RIKEN clone RAFL09-66-B04 (AY099581) as a template

ecotype: Columbia" .. .1511 'gene="At5g13840" 'gene="At5g13840"

/mol\_type="mRNA" /db\_xref="taxon:3702"

/clone="U24960" /chromosome="5"

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TPHKVIDAPSLQDDPYLNVVDWSSQNVLAVGIGTCVYLWTASNSKVTKU.CDLGPNDSV
CSVQWTREGSYISIGTSHGQVQVWDGTQCKRVRTWGGHQTRTGVLAWNSRILSSGSRD
RNILQHDIRVQSDFVSKLVGHKSEVCGLKWSHDDRELASGGNDNQLLVWNNHSQQPIL
                                                                                                 KLTERTAAVKAITWSPHQSSILLASGGGTADRCIRFWATTWGWOLNSIDTGSGVCNLAW
SKOVNEIVSTHGYSQNQIMLMKYPSMSKVATLTGHSMRVLYLATSPDGGTIVTGAGDE
TLRFWNVFPSVKMQTPVKDTGLWSLGRTQIR"
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Best Local Similarity 66.1%; Pred. No. 5.7e-100;
Matches 680; Conservative 0; Mismatches 349;
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Nguyen, M., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers

organism="Arabidopsis thaliana"

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23.5%; Score 472.4; DB 8;
Best Local Similarity 66.1%; Pred. No. 5.8e-100;
Matches 680; Conservative 0; Mismatches 349;
                                                                            thaliana"
                                                                                                                                                                             (R24960)"
                                                                            organism="Arabidopsis"
                                                                                                                                                                             /clone="RAFL09-66-B04
                                                                                                      /mol_type="mRNA"
/db_xref="taxon:3702"
                               Location/Qualifiers
     contributed
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     (SSP/Stanford)
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I (bases I to 1891)

S Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Chung,M.K., Hayashizaki,Y., Banh,Y., Carninci,P., Chen,H., Chenk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakran,T., Sakcu,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

Direct Submission

L Submitted (24-APR-2002) DNA Sequencing and Technology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aroyssi 1891 bp mRNA linear PLN 06-MAY-2002
Arabidopsis thaliana cell cycle switch protein (At5g13840) mRNA,
complete cds.
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                                                                                    GAGGAACTGCAGATAGATGTATTCGTTTTTGGAATACAACCACAAACTCACACGTTAGCT 1301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collection and clustering of RAFL CDNAB (RAFL CDNA): 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1319 GCCAGACTATAGTGACCGGAGCAGGAGATGAGACCTGCCGGGTTTTGGAACGTCTTTCCTT
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RESULT 9 AY099581 LOCUS DEFINITION

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1 (bases 1 to 303)

1 (bases 1 to 303)

Direct Submission

Submitted (22-JAN-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 2082-7510, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis, Similar to frizzy-related protein 1 (Drosophila), clone MGC:53225 IMAGE:5543396, mRNA, complete cds.
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through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 96 Row: k Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
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llarity 66.2%; Pred. No. 3.3e-84;
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                                   GTCCCCTCATCAACATGGCCTTTTGGCTTCAGGGGGGGGCACTGCTGACCGCTGCATCCG 1395
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Drosophila fizzy-related down-regulates mitotic cyclins and is required for cell proliferation arrest and entry into endocycles Cell 90 (4), 671-681 (1997)
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Lebner, C.F.
Submitsed (04-JUL-1997) C.F. Lebner, Department of Genetics,
University of Bayreuth, 95440 Bayreuth, FRG
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/organism="Xenopus laevis"
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Xenopus laevis (African clawed frog)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1861)
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Codon start=1

/codon start=1

/product="Unknown (protein for MGC:55450)"

/db xref="G1:28856200"

/db xref="G1:28856200"

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KILRSPRYPTRISKIPSTPPRABLOFTANLVDWSSLNVLSVGGTCVYLWSACT

SQYTRLCDLSVGGSRDRMILQRDIRTPPLQSERRILGPROSUCGLKWSTDHQLLASGG

NUNKLLWNNSSVLPMQOYTHIAAVVRTHASPYCHIRASPGGGGTADRCIRFWNTLTA

QPLQCIDTGSQVCNLARKSTYRELVSTHGSYSQNGILWWKYPSLTQVAKLTGHSYRVLY

LAMSPDGBAIVTGAGDETIRFWNVFSKTRSTKESVSULNFFRIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                USAN WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi
CDNA Library Preparation: Dr. Sumio Sugano and Michelle Whiting
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                       VRT 05-MAR-2003 complete cds.
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                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
[ (basea 1 to 2089)
Strausberg,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                               Submitted (04-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 101 Row: h Column: 12. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 CCTTATAAGGTTTTGGATGCACCTGCTTTGCAAGATGATTTTTATCTGAATCTGGTAGAT
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/mol_type="mRNA"
/strain="AB.
/strain="AB.
/db.xref="taxon:7955"
/clone="MGC:55450 IMAGB:2639752"
/tissue_type="Whole body, adult, (one male ar including unifertilized eggs)"
/clone lib="Sugano Kawakami zebrafish DRA"
/lab_host="Vector: pME18S-FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 357; DB 5; Length 2089;
Pred. No. 6.7e-73;
0; Mismatches 330; Indels
                                                           2089 bp mRNA linear
Danio rerio, clone MGC:55450 IMAGE:2639752, mRNA,
EC048038
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Danio rerio
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Best Local Similarity 63.4%;
Matches 581; Conservative
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1120 1234 1180 1414

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1480

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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gapbbs-r@mail.nih.gov
Email: gapbbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor Coilege of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.ngsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: I Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 1861

/ Organism="Mus musculus"

/mol type="mgNa"

/strain="FVB/N"

/db xref="taxon:10000"

/clone="MGC:11723 IMAGE:3967009"

/tissue type="mgAmmary tumor. Metallothionien-TGF alpha

model. 10 month old virgin mouse. Taken by biopsy."

/clone="lib="NGI GAPP_Mam"

/lab_host="mblo"

/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="synonym: Fyr"
|db_xref="LocusID:56371"
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'gene="Fzr1"
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Strausberg, R.
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AUTHORS
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1333
/db xref="LocusID:56371"

franslation="MDQDYERRILRQITIONENTVPCVSEMERTLTPANSPVSSPSKH
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LIQCIDYGSQVCRLAWSKHANELVSTHGYSQNQILVWKYPSLTQVAKUTGHSYRVLTGQP
LIQCIDYGSQVCRLAWSKHANELVSTHGYSGNGILVWKYPSLTQVAKUTGHSYRVLTLAG
LGCDTGGGQVCRLAWSKHRSKTRSTKESVSVLANFTRIR"

5 SG G 330 L
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Human homologue of Fizzy-related protein

Published Only in Database (1999)

2. (bases 1 to 1491)

Kotani, S., Oyamatu, T. and Todokoro, K.

Direct Submission

Submitted (129-APR-1998) Kazuo Todokoro, The Institute of Physical
and Chemical Research (RIKEN), Molecular Cell Science Laboratory;

3-1-1, Koyadai, Teukuba, Ibaraki 305-0074, Japan

(E-mail:todokoro@rtc.riken.go.jp, Tel:81-298-36-9075,
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                      GTTCTCTATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATGAA 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2258)
2 (in. D.-Y. and Jeang, K.-T.
Characterization of mouse fizzy*related protein
Unpublished
2 (bases 1 to 2258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>akcekerirerkecirekkeriderekerieerieerekkeriderekeerid</u>
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Direct Submission
Submitted (12-AUG-1998) LMM, NIAID/NIH, 9000 Rockville Pike,
Bethesda, W. 22-0460, USA
Bethesda, Docation/Qualifiers
1. .2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 1.5e-71;
0; Mismatches 338; Indels
                                                                                                                                                                                                                                                 ACCCTGAGGTTCTGGAATGTCTTC 1642
                                                                                                                                                                                                1514 ACGCTTAGGTTCTGGAATGTTTTC 1537
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Best Local Similarity 62.8%;
Matches 580; Conservative
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VTRLCDLSVGDSVTSVGWSRRGNLVAVGTHKGFVQIMDAAGKKLSMLEGHTARVGA
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Pred. No. 4.2e-69;
0; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Fizzy-related protein"
                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                  mol_type="mRNA"
|db_xref="taxon:9606"
| . .1491
                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /gene="fzr1"
1. 1491
/gene="fzr1"
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ilarity 62.8%;
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Fax:81-298-36-9090)
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Search completed: January 23, 2004, 19:53:10 Job time : 7472 secs

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January 23, 2004, 10:49:52 ; Search time 596 Seconds (without alignments) 9085.692 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2552756 seqs, 1349719017 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|    | Description                     | cDNA encoding an a | Human ORFX ORF3013 | Drosophila melanog | Candida albicans e | DNA encoding novel | Aspergillus fumiga | Aspergillus fumiga | Aspergillus fumiga |
|----|---------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|    | ID                              | AAZ37024           | AAC77458           | ABL05493           | ABZ32308           | AAS77749           | ABT18274           | ABT18868           | ABT20688           |
|    | 80                              | 21                 | 21                 | 23                 | 24                 | 23                 | 23                 | 25                 | 25                 |
|    | Query<br>ore Match Length DB II | 2006               | 5905               | 2645               | 1794               | 3940               | 1398               | 1398               | 1875               |
| dе | Query<br>Match                  | 100.0              | 16.9               | 16.7               | 15.1               | 13.4               | 13.2               | 13.2               | 13.2               |
|    | Score                           | 2006               | 339.2              | 334.8              | 303.8              | 269.6              | 263.8              | 263.8              | 263.8              |
|    | Result<br>No.                   | ;<br>;<br>;<br>;   | 7                  | m                  | 4                  | Ŋ                  | 9                  | 7                  | 60                 |

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| Aspergillus fumiga | fumig    | Aspergillus fumiga | Drosophila melanog | Drosophila melanog |          | Drosophila melanog | Drosophila melanog | Arabidopsis thalia | rosophil | Sequence encoding | breast canc | cancer relat | cancer   | Oesophagus cancer | differ   | Human cancer assoc | Seguence encoding | Arabidopsis thalia | Aspergillus oryzae | Drosophila melanog | elan     | (D)      | DNA encoding novel | Human transcriptio | Toxicologically re | Human ovarian canc | Phase-1 Rat CT gen | Human colon cancer | varian can | da albic | ovari    | Human gene express | rentia   | Human ovarian cand | 810      | Human ORF2082 CDNA |        |
|--------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|-------------------|-------------|--------------|----------|-------------------|----------|--------------------|-------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|----------|----------|--------------------|----------|--------------------|----------|--------------------|--------|
| ABT20090           | ABT17680 | ABT19494           | 49                 | ABL18423           | ABL18422 | ABL05448           | ABL07411           | ABZ13183           | ABL07410 | AAQ96099          | ABT11002    | ABL65393     | ABL65837 | ABL67656          | ABK35539 | AAC77801           | AAQ96100          | AAC46256           | AAF11864           | ABL10086           | ABL06722 | ABX83461 | AAS77748           | ABN75375           | ABZ82891           | ABL81366           | ABT09540           | AAH30586           | ABL82189   | m        | ABL81347 | ABZ35113           | ABX77642 | ABL81060           | AAT23988 | 71.3               | 1      |
| 25                 | 25       | 25                 | 23                 | 23                 | 23       | 23                 | 23                 | 24                 | 53       | 16                | 24          | 24           | 24       | 24                | 24       | 21                 | 16                | 21                 | 27                 | 23                 | 23       | 25       | 23                 | 24                 | 52                 | 24                 | 24                 | 21                 | 24         | 24       | 24       | 24                 | 25       | 24                 | 16       | 24                 |        |
| 1993               | 3398     | 3993               | 14283              | 1369               | 3369     | 5058               | 1706               | 1344               | 3852     | 1767              | 1686        | 1686         | 1686     | 1686              | 1686     | 1688               | 1700              | 2697               | 650                | 14482              | 3404     | 274      | 574                | 645                | 1024               | 480                | 672                | 416                | 484        | 1905     | 457      | 469                | 678      | 480                | 310      | 486                | )<br>• |
| 'n                 | ë.       | m                  | ď                  | 3                  | ,        | N                  | H                  | ö                  |          | ö                 |             |              |          |                   |          |                    |                   |                    |                    |                    |          |          |                    |                    |                    |                    |                    |                    |            | 4.6      |          |                    |          |                    |          |                    |        |
| 63.                |          | 63.                | S                  | 4                  | 4        |                    | 31.                | 13                 | 213.2    | 00                | 198.8       | 98           | 86       | 98.               | 98.      | 98                 | 98.               | 91                 | 74                 | 57                 | 52       | Н        | 32                 |                    | 33                 | 6                  | ത                  | 덩                  | 97         | 92.8     | N        | 0                  | 00       | 70                 | 67.8     | ٠,                 |        |
| ov                 | 10       | 11                 | 12                 | 13                 | 14       | 15                 | 16                 | 17                 | 18       | 19                | 20          | 21           | 22       | 23                | 24       | 25                 | 26                | 27                 | 28                 | 29                 | 30       | 31       | 32                 | 33                 | 34                 | 3                  | 36                 | 3.7                | 38         |          | 4        | c 41               | 4        | c 43               | 4        |                    | n<br>r |

## ALIGNMENTS

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Alfalfa; ccc52Ms; WD40 motif; fizzy-related; fzr subfamily; fzr protein; cellular differentiation; endoreplication; cell proliferation; plant cell; somatic embryogenesis; endoploidy; reserve tissue; in vitro plant regeneration; ss.
                                                                             cDNA encoding an alfalfa fzr protein designated ccc52Ms.
                                                                                                                                                                      Location/Qualifiers
182..1609
/*tag= a
/product= "ccc52Ms"
                   AAZ37024 standard; cDNA; 2006 BP.
                                                                                                                                                                                                                                                                   98FR-0007174.
                                                                                                                                                                                                                                                                                       98FR-0007174.
                                                            13-MAR-2000 (first entry)
                                                                                                                                                       Medicago sativa.
                                                                                                                                                                                                                                                                    08-JUN-1998;
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                                                                                                                                                                                                                            FR2779433-A1
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                                       AAZ37024;
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RESULT 1
          AAZ37024
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WPI; 2000-089743/08. P-PSDB; AAY53985. Kondorosi E, 

Disclosure; Page 21-23; 36pp; French.

New plant protein, useful for regulating differentiation and proliferation of plant cells, especially for stimulation of somatic embryogenesis

Kondorosi A;

Cebolla A,

The present sequence encodes an alfalfa protein, designated ccc52Ms.

The protein contains repeated WD40 (Trp-Asp) motifs, and belongs to the far (fizzy-related) subfamily. The WD40 motifs are situated in the central portions and the C-terminal portion of the protein. The protein comprises 7 domains, and the last domain, domain 7, contains a potential liaison site for cyclims. The N-terminal region of the protein has a peptide sequence (DRFIPSR) which corresponds to a motif which is conserved in fir proteins. The protein intervenes in the regulation of cellular differentiation, and augments endoreplication. The polymuclocitide sequence and its antisense sequences are used to regulate the differentiation and proliferation of plant cells and for stimulating somatic embryogenesis. They are also useful for promoting conditions and its in vitro regeneration of plants from central sources, and to stimulate in vitro regeneration of plants from callus in culture, by increasing the conversion of embryos.

Sequence 2006 BP; 555 A; 398 C; 441 G; 612 T; 0 other;

Query Match

120 120 180 180 9 9 121 TGCAAAAATTCTTTTACAGCGTTCTTTTTTCCCCCGGGAAAAAATTAACACAGCTCCGC TGCAAAAAATTCTTTTACAGCGTTCTTTTTCCCCGGGAAAAAATTAACACAGCTCCGC 0; Gaps 100.0%; Score 2006; DB 21; Length 2006; 100.0%; Pred. No. 0; Alsmatches 0; Indels 0; Best Local Similarity 100.0 Matches 2006; Conservative 121 61 61 ઠે 셤 ઠે ď ò 셤

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CATGGACGGAACCGGTAATCGAAATCCACCGACTTCCACCGTCAGAGACAATTCTCC

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                                                                                                                                                                                                                                                                                                                                                                 Human, open reading frame, ORFX, detection, cytostatic; hepatotropic;

wulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective;
wulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective;
muticonvulsant; offeropathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
whypotensive; dermatological; immunosuppressive; antidiabetic;
mutical antibacterial; antifungal; antithematic; antithyroid;
mutical terrative disorder; osteoarthritis; areft vs host disease;
mutical ar disease; diabetes mellitus; hypothyroidism; SCID; ALDS;
cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
mullengy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
bone danage; contraceptive; ss.
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                                         TTTACCAACTGGGAGAGCCTTGGAGGGAGCTATAAAAGTTTTGATATGGCTGCCGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF3013 polynucleotide sequence SEQ ID NO:6025.
                                                                                                                                                                                                             TAACAGAGAAAAAAAAAAAAAAA 2006
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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P-PSDB; AAB43249.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities uch as: oyfostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; antiparkinsonian; nootropic; neuroprotective;
continuostimulant; cardiant; thrombolytic; coagulant; vasotropic;
immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic, hypotensive; dermatological; immunosuppressive;
antidiabetic, hypotensive; dermatological; antifungal; antirheumatic;
antidiapetic, hypotensive; dermatological; immunosuppressive;
continuostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiapetic, hypotensive; dermatological; immunosuppressive;
coagulation; hypothyroidism condition associated with an ORTX-associated disorder. The
nucleic acides can be used to express ORFX proteins in gene therapy,
cetors. The proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
graft vs host disease, cardiavascular disease, diabetes mellitus,
cythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
bacterial or fungal infection, malaria, autoimmune disorders, asterma,
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
coagulation; to inhibit thrombosis; and as a contraceptive.
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Best Local Similarity 62.7%; Pred. No. 1.8e-68;
Matches 562; Conservative 0; Mismatches 328; Indels
5; Page 5206-5209; 5507pp; English
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1384 GGCGGCACAGCTGACCGCTGTATCCGCTTCTGGAACACGCTGACAGGACAACCACTGCAG 1443
                         TGTATGGACACTGGAAGTCAGGTTTGCAATCTTGTTGGTCCAAAAATGTCAACGAACTA 1360
                                                 1444 TGTATCGACACGGCTCCCAAGTGTGCAATCTGGCCTGGTCCAAGCCACGCCAACGAGCTG 1503
                                                                           GTAAGCACACATGGGTACTCCCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCA 1420
                                                                                              1421 AAGCTGGCGACTCTTACCGGCCATACTTATAGGGTTCTCTATATCTTGCCATCTCTCCAGAT 1480
                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeuticis and pharmaceutical furge. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01800-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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16.7%; Score 334.8; DB 23; Length 2645; Second Best Local Similarity 61.5%; Pred. No. 1.5e-67;
Matches 572; Conservative 0; Mismatches 352; Indels 6; Gaps
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                                                                                                                                                                                                   1624 GGGGAGGCCATCGTCACTGGTGCTGGAGACACCCTGAGGTTCTGGAACGTCTT 1679
                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 10961.
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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P-PSDB; ABB61390.
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                                                                                                                                                  674 TIGCAAGAIGAITITIAICIGAAICIGGIAGAITGGICTICACACAAIGIGITGGCIGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion; of a promoter replacement fragment with a heterologous recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulares the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional compound catabolism, biosynthetic, transporter, transcriptional contraint, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential candida albicans gene used in the method of the invention. Note: The sequence data for this patent is not represented in the printed the brown parent of the present of the printed of the invention.
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                                                    Pungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Constructing strains for identifying gene products as effective for therapeutic intervention, by inactivating in the strain one of a gene and placing other allele of the gene under conditional expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Score 303.8; DB 24; Length 1794; 58.1%; Pred. No. 2e-60; ive 0; Mismatches 387; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 37; SEQ ID NO 6595; 167pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL;
                       Candida albicans essential gene SEQ ID NO 6595
                                                                                                                                                                                                                                                                                                                                                                  Bussey H,
                                                                                                                                                                                                                                                                                                                                                                  Boone C,
                                                                                                                                                                                                                                                            29-DEC-2000; 2000US-259128P.
20-FEB-2001; 2001US-0792024.
22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                26-DEC-2001; 2001WO-US49486.
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Matches 536; Conservative
                                                                                                                                                                                                                                                                                                                                 (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                  Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-566694/60.
P-PSDB; ABP73758.
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                                                                                                                            Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                   Roemer T,
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Best Local 9
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                                                                                                                                                                                                                                                                                                                     GCTGTTGGAACTAACAATGGTAAAGTTCAGATTTTGGGATGCAGGAAGAAGAAGATA
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794 GATTIGGGGGTIGATGATIGIFFIGITICITIGGTIGGGCTCAACCIGGTACTCAICTT
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CTATTGCATGGTCTCCTCATCATGGACTTCTTGCATCTGGAGGAACTGCAGATA 1256
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27-APR-2001; 2001US-287066P.
05-UTN-2001; 2001US-295890P.
09-UTL-2001; 2001US-303899P.
31-AUG-2001; 2001US-316362P.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences.
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llarity 62.6%; Pred. No. 2.1e-52;
Conservative 0; Mismatches 259; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 13553; 103pp; English
                                                                                                                                                                                          Tang YT;
                                                    30-MAR-2001; 2001WO-US08631.
                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                              WPI; 2001-639362/73.
                                                                                                                                                                                          Liu C,
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                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                   P-PSDB; ABG13562.
                                                                                                                                                                                          Drmanac RT,
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Best Local Similarity 56.3%; Pred. No. 3.4e<sup>o</sup>
Matches 557; Conservative 0; Mismatches
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27-APR-2001; 2001US-287066P.
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09-JUL-2001; 2001US-303899P.
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similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymoclectides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
13.2%; Score 263.8; DB 25; Length
Best Local Similarity 56.3%; Pred. No. 3.4e-51;
Matches 557; Conservative 0; Mismatches 372; Indels
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fundatus. The isolated nucleic acids of essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat or prevent infections by absthogranic organism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or inhibit formation on a surface of a by A. fundatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fundatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. fundatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA similar orthologous essential or virulence genes, for selecting and potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination
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Aspergillus funigatus, useful for treating or preventing infections
A. funigatus, or for treating a non-infectious disease in a subject
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27-APR-2001; 2001US-28766F.
05-UUN-2001; 2001US-295890P.
09-UUL-2001; 2001US-318399P.
31-AUG-2001; 2001US-316362P.
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of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for isolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention.
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Best Local Similarity 56.3%; Pred. No. 3.7e-51;
Matches 557; Conservative 0; Mismatches 372; Indels
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1875 BP; 514 A; 490 C; 464 G; 407 T; 0 other;
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of other related or distant pathogenic crosmoraling with DNA similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential or virulence genes, for sequences for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifyling polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding
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27-APR-2001; 2001US-287066P.
05-UTN-2001; 2001US-295890P.
09-UTN-2001; 2001US-3163899P.
31-AUG-2001; 2001US-316362P.
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interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to stolate correlative receptors or ligands in the case or virulence factors. This polymucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention.
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Mismatches 372;
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Best Local Similarity 56.3
Matches 557; Conservative
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a capterism of a proper or inhibit formation on a surface of a capterism of a fumigatus. The polymucleotides are useful for captesing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify making oligomers for a distant pathogenic organisms to identify making oligomers for a factorial and a nucleic acid array for examination making oligomers for a factoriant to a nucleic acid array for examination
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                              essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
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ATAGGGTTCTCTTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAG
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Aspergillus fumigatus, useful for treating or preventing infections
A. fumigatus, or for treating a non-infectious disease in a subject
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2001US-295890P.
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                                                                                                                                                                                                                                                                                                                                                                                  Pungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tishkoff D,
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of
                                                                                                                     Sequence 3398 BP; 884 A; 845 C; 789 G; 880 T; 0 other;
isolate correlative receptors or ligands in the case factors. This polynucleotide sequence represents one genes of Aspergillus fumigatus of the invention.
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fundatus. The isolated nucleic acids of the invention are used to treat or prevent infectious by a pathogenic corganism such as A. fundatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or inhibit formation on a surface of a cobject (e.g. cancer), to prevent or inhibit formation of an object of therapeuts out or prevent or inhibit formation of an object of comprising recombinant protein for characterisation, screening or therapeuts use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. fundatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify operation or distant pathogenic organisms to identify of comparing or distant pathogenic organisms to identify of comparing or distant pathogenic organisms to identify of antipodies, as an antipen to raise anti-DNA antibodies or to elicit another immune crespones, as a reagent in assays designed to quantitatively determine levels of the protein in sasays designed to quantitatively content or interaction. The polypeptides may be used to raise antibodies and to host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polymuleocide sequence represents one of the essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response; ds.
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Aspergillus fumigatus, useful for treating or preventing infections
A. fumigatus, or for treating a non-infectious disease in a subject
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                                       fumigatus essential gene #1852.
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27-APR-2001; 2001US-287066F.
05-UUN-2001; 2001US-295890P.
09-UUL-2001; 2001US-303899F.
31-AUG-2001; 2001US-316362P.
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                                                                                     DB 25; Length 3993;
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Sequence 3993 BP; 1049 A; 991 C; 913 G; 1040 T; 0 other;
                                                                                Score 263.8; DB 25;
Pred. No. 4.7e-51;
0; Mismatches 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 10958
                                                                                                                                                             developmental biology, cell signalling, insecticide,
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12.9%; Score 259; DB 23; Length 1
Best Local Similarity 60.4%; Pred. No. 9.3e-50;
Matches 446; Conservative 0; Mismatches 290; Indels
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLO1840 ABLIG175) and the encoded proteins (ABBS7737-ABB72072). The sequence acts for this patent did not form part of the printed specification, but was obtained in electronic format directly from without fire, wipo.int/pub/published_pct_sequences.
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| 0000000000000000000   |        | 956B-1<br>1, Application US/<br>1, 6291642<br>INFORMATION:<br>INFORMATION:<br>Weinstein, Jasm<br>F INVENTION: NO. 62<br>FREENCE: 06843.0026<br>APPLICATION NUMBER<br>APPLICATION DATE: 1997<br>DF SEQ ID NOS: 31<br>2: Patentin Ver: 2.'.<br>2: 1767<br>NN. A.   | ilari<br>Cons                 |  | TGA   | TGA   | AE S   |   | <br>GAGCAG        | 7GG/                            | 999  | PA S   | TGG1   | FG<br>FG<br>FG  |
| 4   |        | 956B-1<br>1, App<br>1, App<br>1, 6291<br>MYCRM<br>WT: Wei<br>WT: Wei<br>TIVE<br>APPLIC<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FILING<br>FI | h<br>Simil.<br>88; C          | \$ <del>-</del> 8  |   | σ   | 0 0  | ე   | - 6<br>G          |                                 | 9<br>GT  | 7 F  | 7 TC   | on.   |
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| B00100400000010040  |        | SEULT 1 S. 08-988-856 Sequence 1, Patent No. GENERAL INN. APPLICANT TITLE OF 1 FILE REFER CURRENT AR CURRENT PROPRESSE SEQ ID NO. LENGTH: 1 LENGTH: 1 LENGTH: 1 LENGTH: 1 CREANISM. CREANISM. CREANISM. CORGANISM.   | C 73                          |  |   |   |  |   |                   |                                 |  |  |  |   |
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GENERAL INFORMATION:
APPLICANT: Weinstein, Jasminder
TITLE OF INVENTIONS: Novel Mammalian Cell Cycle Protein
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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AMORE INC./Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01806
FILING DATE:
CLASSIFICATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
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, LOCATION:
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Query Match

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   Pred. No. 9.7e-42;
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Parent No. 6291642
GENERAL INFORMATION:
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Conservative (
Best Local Similarity
Matches 488; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Weinstein, Jasminder
APPLICANT: Weinstein, Jasminder
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDERSE: Amgen Inc./Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC comparatible
COMPUTER: LEW PC comparatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01806
FILING DATE:
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.9%; Score 198.8; DB 5; 52.7%; Pred. No. 2.4e-41; ative 0; Mismatches 422;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1700 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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Best Local Similarity 52.7
Matches 487; Conservative
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PCT-US95-01806-3
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PCT-US95-01806-3
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                              TITLE OF INVENTION: No. 6291642el Mammalian Cell Cycle Protein FILE REFERENCE: 06643.0026-04; A-283 D CURRENT APPLICATION NUMBER: US/08/989,856B CURRENT FILING DATE: 1997-12-11 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 1700
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al Similarity 52.7%; Pred. No. 2.4e-41;
487; Conservative 0; Mismatches 422;
               APPLICANT: Weinstein, Jasminder
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Sequence 6283, Application US/09313294A

Batent No. 6476212

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILLE OF INVENTION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
                                           GCTGTATGGACACTGGAAGTCAGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAAC 1358
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Sequence 1, Application US/08204675

GENERAL INFORMATION:

APPLICANT: Boeke, Jef D.

APPLICANT: Braiterman, Lelita T.

TITLE OF INVENTION: In Vitro Transposition of Artificial

TITLE OF SEQUENCES: 7

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE Banner, Birch, McKie, and Beckett
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; OTHER INFORMATION: Incyte ID No. 6476212 700351538H1
US-09-313-2944-6283
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
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SEQ ID NO 6283
LENGTH: 288
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Sequence 1921, Application US/09313294A
Patent No. 647612
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lolura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT PILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOCTWARRE: PERL PROGRAM
SEQ ID NO 1921
LENGTH: 274
963 AGTGGTTCACGTTCTGGCCACATCCACCACCATGATGTTCGGGTAGCAGAACACCATGTG 1022
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CTHER INFORMATION: Incyte ID No. 6476212 700551746H1

NAME/KEY: unsure

LOCATION: 22, 41, 47, 49, 53

COTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-1921
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ORGANISM: Zea mays
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CURRENT APPLICATION DATA:
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1 Sequence 1, Application US/08660754

2 Patent No. 5843772

GENERAL INFORMATION:

APPLICANT: Boeke, Jef D.

APPLICANT: Braiterman, Lelita T.

TITLE OF INVENTION: In Vitro Transposition of Artificial

TITLE OF INVENTION: Transposons

NUMBER OF SEQUENCES:

ADDRESSEE: Banner, Birch, McKie, and Beckett

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARING SYSTEM: PC-DOS/MS-DOS

SOFTWARING SYSTEM: PC-DOS/MS-DOS

SOFTWARING SYSTEM: BC-DOS/MS-DOS

GURSENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,675

FILING DATE: O2-MAR-1994

CLASSIFICATION: A355

ATTORNEY/AGENT NUMBER: 32,141

RESISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.45501

TELEPAN: 202.508.919

TELEPAN: 202.508.919

TELEPAN: 202.508.919

TELEPAN: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CRARACTERISTICS:

LENGTH: 4164 base pairs

TYPE: MCGHEN CALCALLARIES

TOPOLOGY: CITCULARIES

TOPOLOGY: CITCULARIES

TOPOLOGY: CITCULARIES
                                                                                                                                                                                                                                                                                                                                                                                                                          UOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
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; Sequence 1, Application US/08796364
; Sequence 1, Application US/08796364
; Sequence 1, Application US/08796364
; GENERAL INFORMATION:
; APPLICANT: Boeke, Jef D.
; APPLICANT: Braiterman, Lelita T.
; TITLE OF INVENTION: Transposons
; TITLE OF INVENTION: Transposons
; VINEER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 & Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
CURRENT APPLICATION DAIA:

APPLICATION NUMBER: US/08/660,754
FILING DATE:
CIASSIPTCATION: 435
FILING DATE:
TILING DATE:
TOZNEN' AGENT INFORMATION:
NAME: RAGAN, SATAN A.
REGISTRATION NUMBER: 32,141
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COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 AAAA 2005
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IMMEDIATE SOURCE:
CLONE: PAT-1
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HYPOTHETICAL: NO
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US-08-204-675-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46.4; DB 2; Length 4164;
Pred. No. 0.035;
0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9502520
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Banner, Birch, McKie, and Beckett STREET: 1001 G Street, N.W. CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPPRATIG SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US95/02520
FILING DATE: 02-MAR-1995
CLASSIFICATION:
 PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MRR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SATA A.
REFERENCE/DOCKET NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.455/
TELECHONNICATION INFORMATION:
TELEPHONNICATION INFORMATION:
TELEFAK: 197430 EBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENGTH: 4164 base pairs
TENGTH: 4164 base pairs
                                                                                                                                                        01107.45501
APPLICATION NUMBER: US/08/796,364
                                                                                                                                                                                                                                                                                                                        . TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.33
Matches 98; Conservative
                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                 HYPOTHE. NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002 AAAA 2005
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RESERRECT NUMBER: 02107.49245

RESTREMENTION NUMBER: 02107.49245

TELEPRONEIN CONCETN NUMBER: 02107.49245

TELEPRONEIN CONCETN NUMBER: 02107.49245

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TOTAL GOT 50
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FILING DATE:
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US. OB-66.0754-Z
US. OBPLIANCEMATION:

APPLICANT: Devine, Scott E.

APPLICANT: Braiterman, Lelita T.

TILE OF INVENTION: In Vitro Transposition of Artificial
TILE OF INVENTION: In Vitro Transposition
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner, Birch, McKie, and Beckett
STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20001
COMPUTER: PREADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IN PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,754
FILING DATE: US-MAR-1994
ATTORNEY/AGENT INFORMATION:
NEARE: MEDIAL MATHORDED:
PLING DATE: STATE APPLICATION NUMBER: US/08/675
FILING DATE: US/08/675
NUMBE: MAGNATION: WAS APPLICATION NUMBER: US/08/675
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%; Score 46.4; DB 1; Length 4933;
53.3%; Pred. No. 0.037;
tive 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 01107.45501
TELECOMMINICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEX: 197430 BENB UT
TELEX: 197430 BENB UT
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.33
Matches 98; Conservative
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; IMMEDIATE SOURCE:
; CLONE: PAT-2
US-08-204-675-2
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US-08-660-754-2
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; Sequence 2, Application US/08796364
; Sequence 2, Application US/08796364
; Sequence 2, Application US/08796364
; APELICANT: Devine, Scott E.
; APELICANT: Brake, Jef D.
; APPLICANT: Brake, Jef D.
; APPLICANT: Brake, Jef D.
; TILLE OF INVENTION: In Vitro Transposition of Artificial
; TILLE OF INVENTION: Transposons
; UNDERSORE: 3
; CORRESPONDENCES: 7
; CORRESPONDENCES: 7
; CORRESPONDENCES: 7
; CORRESPONDENCES: 8
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                  Length 4933;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.3%; Score 46.4; DB 2; Length 4
Best Local Similarity 53.3%; Pred. No. 0.037;
Matches 98; Conservative 0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAIR: "D.C. COUNTRY: U.S.A. ZIP. 20001.
ZIP: 20001.
COMPUTER READABLE FORM:
WINDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPAIRE: IBM PC COMPAIRE: BM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DARROWS. US/08/796,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: KAGEN: SATEM 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELEPHONE: 202.508.9100
TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEY: 1974-30 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-2
US-08-660-754-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002 AAAA 2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: plasmid US-09-890-848-16
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                                                                                                                                                       Score 46.4; DB 5; Length 4933; Pred. No. 0.037; 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09890848
; Sequence 16, Application US/09890848
; Patent No. 6573053
; GENERAL INFORMATION:
APPLICANT: Fitth, Greg
; APPLICANT: Fitth, Greg
; TITLE OF INVENTION: Analysis Method
; TITLE OF INVENTION: Analysis Method
; FILE REFERENCE: PA9903
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: ET/GB00/00346
; PRIOR APPLICATION NUMBER: EP/CFG00/00346
; PRIOR APPLICATION NUMBER: EP/CFG00/00346
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 16
; LENGTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
                  DNA (genomic)
NO
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ORGANISM: Artificial Sequence
                                                                                                                                                            Query Match
Best Local Similarity 53.3%;
Matches 98; Conservative (
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               MOLECULE TYPE: DNP
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-2
PCT-US95-0250-2
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US-09-890-848-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4610 CTTÁTCGTTAÁTCGÁÁTGTÁTGTÁTTTÁATCTGCTÍTTCTTGTCTAATÁAATÁTÁTÁT 4669
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Sequence 2, Application PC/TUS9502520

GENERAL INFORMATION:

TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Iransposition of Artificial
TITLE OF INVENTION: Transposition of Artificial
TOTHER OF INVENTION:

CORPESSOR SEQUENCE:

COUNTRY: Washington
STATE: D.C.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: INP PC Compatible
OPERATING SYSTEM: PCTOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:

APPLICATION NUMBER: PCTUS95/02520
FILING DATE: D2-MAR-1995
SUTCHARL AREALING
                                                                                                                                                                                                                                                                                                               Score 46.4; DB 2; Length 4933;
Pred. No. 0.037;
0; Mismatches 86; Indels 0
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NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.49245
TELECOMMUNICATION INFORMATION:
TELEFPAX: 202.508.9299
TELEFX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: INCleded acid
STRANDEDNESS: double
TOPOLOGY: circular
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4933 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
INMEDIATE SOURCE:
CLANT. - XXXX
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3%;
Matches 98; Conservative
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US-08-796-364-2
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Search completed: January 23, 2004, 21:08:23 Job time : 142 secs

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January 23, 2004, 19:53:14; Search time 713 Seconds (without alignments) 10062.272 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*

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7/cgn2_6/ptodata/2/pubpna/DTO8_NEW PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

15: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

16: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*

17: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/USO0_NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2356869 seqs, 1788235258 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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2006
                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description      | 27884, A    | 6595, Ap            | 26005, A           | 26011, A            | 26013, A            | 36526, A            | 1038, Ap            | 2038, Ap           | 7038, Ap           | 6038, Ap           | 38, Appl           | 5038, Ap         | 45642, A           | 988, App            | 988, App           |                    |
|------------------|-------------|---------------------|--------------------|---------------------|---------------------|---------------------|---------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|---------------------|--------------------|--------------------|
|                  | Description | Sequence            | Seguence           | Sequence            | Sequence            | Sequence            | Sequence            | Sequence           | Sequence           | Sequence           | Sequence           | Seguence         | Seguence           | Sequence            | Sequence           | Sequence           |
|                  | qı          | US-10-369-493-27884 | US-10-032-585-6595 | US-10-369-493-26005 | US-10-369-493-26011 | US-10-369-493-26013 | US-10-369-493-36526 | US-10-128-714-1038 | US-10-128-714-2038 | US-10-128-714-7038 | US-10-128-714-6038 | US-10-128-714-38 | US-10-128-714-5038 | US-10-369-493-45642 | US-09-938-842A-988 | US-09-938-842A-988 |
|                  | DB          | 12                  | 13                 | 12                  | 12                  | 12                  | 12                  | 15                 | 15                 | 15                 | 15                 | 15               | 15                 | 12                  | 10                 | 12                 |
|                  | Length      | 1143                | 1794               | 1312                | 1312                | 1312                | 1116                | 1398               | 1398               | 1875               | 1993               | 3398             | 3993               | 1701                | 1344               | 1344               |
| * 61<br>91<br>91 | Match       | 16.3                | 15.1               | 13.8                | 13.8                | 13.8                | 13.2                | 13.2               | 13.2               | 13.2               | 13.2               | 13.2             | 13.2               | 11.2                | 10.6               | 10.6               |
|                  | Score       | 326.2               | 303.8              | 277                 | 277                 | 277                 | 264.6               | 263.8              | 263.8              | 263.8              | 263.8              | 263.8            | 263.8              | 225.6               | 213.6              | 213.6              |
| 7 tined          | No.         |                     | ~                  | e                   | 4                   | Ŋ                   | 9                   | 7                  | 80                 | σ                  | 10                 | 11               | 12                 | 13                  | 4                  | 15                 |

| Sequence 25788, A Sequence 1, Appli sequence 107, Appli Sequence 107, Appli Sequence 103, Appli Sequence 1147, Appli Sequence 19, Appli Sequence 19, Appli Sequence 2441, A Sequence 258, Appli Sequence 12508, Appli Sequence 12508, Appli Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 25412, A Sequence 225, Appli Sequence 1259, Appli Sequence 1259, Appli Sequence 225, Appli Sequence 225, Appli Sequence 176, Ap | ,                     |
|--|-----------------------|
|  | CSO/-94-00-101-00-100 |
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| 11111111111111111111111111111111111111   | 4.<br>V               |
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## ALIGNMENTS

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Sequence 6595, Application US/2003018095341

GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.1
SEQ ID NO 5595
                                                                                                                                   1006
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                                            484 ridegariectroagaaagcaaagagcriaagaaccaigacridectrogcaggariedaa
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      58.1%; Pred. No. 3.6e-66; ive 0; Mismatches 387; Indels
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; Sequence 26005, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                           Conservative
Best Local Similarity
Matches 536; Conserv
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greyory J.
APPLICANT: Gladman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXRRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52022) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
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Pred. No. 1.9e-59;
); Mismatches 390;
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US-10-369-493-26011
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                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 26005
LENGTH: 1312
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Pred. No. 1.9e-59;
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CRGANISM: Schizosaccharomyces pombe
US-10-369-493-26005
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Best Local Similarity 56.7%;
Matches 511; Conservative
                 Yongwei
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US-10-36526

US-10-36526, Application US/10369493

Sequence 36526, Application US/10369493

Sequence 36526, Application US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Blater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: 2003-02-28

CURRENT PILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
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## Sequence 26013, Application No. US20030233675A1

### Sequence 26013, Application No. US20030233675A1

### GENERAL INFORMATION:

### APPLICANT: Chory You gregory J.

### APPLICANT: Slater, Steven C.

### APPLICANT: Glodman, Barry S.

### APPLICANT: Glodman, Barry S.

### APPLICANT: Chory Xianfeng

### TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES

### TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION INTERER: US/10/369,493

### CURRENT FILING DATE: 2003-02-28

### PRIOR FILING DATE: 2003-02-21

### NUMBER OF SEQ ID NOS: 47374

### TITLE OF INVENTION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION INTERER: US/10/369,493

### PRIOR PRILING DATE: 2003-02-21

### NUMBER OF SEQ ID NOS: 47374

### TITLE OF INVENTION OF MICROBIAL PROTEINS IN PLANTS FOR PRIOR FILING DATE: 2002-02-21

### NUMBER OF SEQ ID NOS: 47374

### TITLE OF INVENTION INTERER: US/10/360,039
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US-10-369-493-36526
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                                                                                             APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Eroshkin, Alexey M
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
APPLICANT: Lemieux, Sebsatien M
APPLICANTON: Methods of Use
TITLE OF INVENTION: UMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION WUMBER: US 60/285,890
PRIOR PLILNG DATE: 2001-06-05
PRIOR PLILNG DATE: 2001-06-05
PRIOR PLILNG DATE: 2001-06-05
PRIOR APPLICATION WUMBER: US 60/316,362
PRIOR APPLICATION WUMBER: US 60/316,362
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Pred. No. 4.3e-56;
); Mismatches 372; Indels 60;
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US-10-128-714-1038
Sequence 1038, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-1038
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Best Local Similarity 56.3%;
Matches 557; Conservative
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 1038
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                                    ATAGICCGGTTAAGGCTCCTAGGAAGGTTCCTCGATCGCCTTATAAGGTTTTGGATGCAC
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US-10-128-714-7038
; Sequence 7038, Application US/10128714
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US-10-128-714-2038

Sequence 2038, Application US/10128714

Publication No. US20030119013A1

GENERAL INFORMATION:
APPLICANT: Jiang, Bo

APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Lemienx, Sebastien M

APPLICANT: Lemienx, Sebastien M

APPLICANT: Lemienx, Sebastien M

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APPLICANT: Lemienx, Sebastien M

APPLICANT: Lemienx Wenthode of Use
FILIS OF INVENTION: Methode of Use
FILIS PERFENCE: 1018-018-999

CURRENT APPLICATION NUMBER: US 60/285,697

PRIOR APPLICATION NUMBER: US 60/285,697

PRIOR PILING DATE: 2001-04-23

PRIOR FILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

PRIOR PILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 8603

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Query Match
13.2%; Score 263.8; DB 15; Length 1398; Sectional Local Similarity 56.3%; Pred. No. 4.3e-56;
Matches 557; Conservative 0; Mismatches 372; Indels 60; Gaps
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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
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APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TILE REFERENCE: 1018-018-999
CURRENT APPLICATION NUMBER: US 60/285,697
FRIOR PILING DATE: 2001-04-23
FRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR PILING DATE: 2001-06-05
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR PILING DATE: 2001-08-31
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR PILING DATE: 2001-08-31
SOFTWARE: Patentin version 3.1
SEQ ID NO 6038
LENGHH: 1993
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Pred. No. 5.3e-56;
0; Mismatches 372;
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Pred. No. 5.1e-56;
0; Mismatches 372;
                                                          APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essent
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: 1018-018-099
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR PLING DATE: 2001-04-27
PRIOR PELING DATE: 2001-04-28
PRIOR PLING DATE: 2001-04-29
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PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PLING DATE: 2001-07-09
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Best Local Similarity 56.3%;
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          No. US20030119013A1
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APPLICANT: Broshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE PEPERROE: 10182-018-99
GURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,890
PRIOR PILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR PILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/316,362
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PRIOR APPLICATION NUMBER: US 60/316,362
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-38
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Best Local Similarity 56.3%;
Matches 557; Conservative (
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                                                  CCGATTTGCAAGATGATTTCTACTTGAATCTGGTGGACTGGGGCCAGTAGTAATGTGCTAG 1055
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       Length 3398;
Score 263.8; DB 15; Length
Pred. No. 7.2e-56;
0; Mismatches 372; Indels
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Sequence 38, Application US/10128714; Publication No. US20030119013A1; GENERAL INFORMATION: APPLICANT: Jiang, Bo APPLICANT: Hu, Wenqi; APPLICANT: Tishkoff, Daniel

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Sequence 45642, Application US/10369493

Publication No. US20030233675A1

Publication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Galter, Seeven C.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REPERENCE: 38-10 (52052) B
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APPLICANT: Jiang, Bo

APPLICANT: Tishoff, Daniel

APPLICANT: Tishoff, Daniel

APPLICANT: Tishoff, Daniel

APPLICANT: Zamudio, Carlos

APPLICANT: Zamudio, Carlos

APPLICANT: Lemieur, Sebastien M

APPLICANT: Lemieur, Sebastien M

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APPLICANT: Lemieur, Sebastien M

APPLICANT: NUMBRE: U0182-018-999

FILIE OF INVENTION: Methods of Use

FILE REFRENCE: 10182-018-999

CURRENT PILING DATE: 2001-04-23

FRIOR APPLICATION NUMBRE: US 60/285,697

PRIOR PILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-04-27

PRIOR PILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: US 60/295,890

PRIOR PILING DATE: 2001-06-05

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0; Mismatches 372; Indels
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9-10-128-714-5038
; Sequence 5038, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
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                                                                                                                                 Score 225.6; DB 12;
Pred, No. 2.3e-46;
), Mismatches 434;
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                ORGANISM: Saccharomyces cerevisiae
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ilarity 53.3%;
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SEQ ID NO 45642
LENGTH: 1701
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pred. No. 2.2e-43;
0; Mismatches 409;
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Arabidopsis thaliana
US-09-938-842A-988
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Best Local Similarity 54.2%;
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Search completed: January 23, 2004, 23:19:37
Job time : 721 secs
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| Publication No. US20040009476A9
| Publication No. US20040009476A9
| GENERAL INFORMATION:
| APPLICANT: Harper, Jeff
| APPLICANT: Kreps, Joel
| APPLICANT: Kreps, Joel
| APPLICANT: Anny, Xun
| APPLICANT: Zhu, Tong
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| FILE REFERENCE: SCRIP1300-3
| CURRENT FILING DATE: 2001-08-24
| PRIOR APPLICATION NUMBER: US 60/264,647
| PRIOR PLING DATE: 2001-01-16
| PRIOR FILING DATE: 2001-06-22
| NUMBER OF SEQ ID NOS: 5379
| SEQ ID NOS: 5379
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                        Indels 24; Gaps
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Best Local Similarity 54.2%; Pred. No. 2.2e-43;
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ORGANISM: Arabidopsis thaliana
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AY112458 Zea maye BG044933 saa35602.
BG044931 saa35602.
BG044374 GA\_Ba002
CB44274 GA\_Ba002
CB828401 LjABST8865
CB828401 LjABST8865
CB873263 MCT003C07
CB873263 MCT003C07
CA837263 MCT003C07
AA498616 AA498616
CA764180 AA53-KPL
AW055317 614059806
AX08368 Mus muscu
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AX08368 Mus muscu
CA02848 EST0169 N
BB32996 S03299431
BB32996 S03299431
BB32996 S0346804
BB394176 CB840007
BB153551 60244731
BT153551 6024773
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BT154501 60317445
CCD03026 EST1084
CCD03026 EST1084
CCA22075 MTUTTL. PS
BM945914 UI -M-EM0-CB979227 CA840007

Medicago truncatula/Glomus versiforme mixed EST library
Medicago truncatula/Glomus versiforme mixed EST library
ESM Medicago truncatula/Glomus versiforme mixed EST library
EUkaryota; mixed EST libraries.

1 (bases 1 tc 759)
EL tc 759)
EST from roote of Medicago truncatula after colonization with
Glomus versiforme, 2001
Unpublished
Contact: Harrison M.J.

1 Unpublished
Contact: Harrison M.J.

1 Unpublished
ESM Noble Parkway, Ardmore, OK 73401
Tel: 580-221-5810
Fax: 580-221-7380
Email: MiharrisonGhoble.org
Noble EST name: N379566 # TIGR sequence name: MTDBM09TK More
information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC). BG584091

EST485851 MHAM Medicago truncatula/Glomus versiforme mixed EST ll-APR-2001 Library cona clone pMHAM-14B17 5' end, mRNA sequence.

EG584091.1 GI:13599155

BG584091 EST485851 CA919262 EST636980 BIZ70288 NF006A08F BQ146406 NF069G04F

BG584091 CA919262 BI270288 BQ146406

1212

759 820 630 594

33.3 31.1 30.9 28.7

667.2 624.6 620.6 575.4

В

Length

Query

Score

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Description

ALIGNMENTS

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1391
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                                                                                                                                                                                                                              Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledona; core eudicots; rosida
; eurosida I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                 CA919262
BST636980 MTUS Medicago truncatula cDNA clone MTUS-11B5, mRNA
Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            702
                                                                                                                                                                                                                                                                                         1 (bases 1 to 820)
VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 6K unique set: cDNA clones selected and reservayed from various libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 5510
Tel: 612 624 2755
Fax: 612 625 1738
Bax: 612 625 1738
Baxi: kandenbecbs.umn.edu
TIGR sequence name: WTUAKL/TV
More information is available at: www.medicago.org
Seq primer: (9tA Ath CgA CCC Act Ath 999 C).
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94.9%; Pred. No. 1.1e-72;
.ive 0; Mismatches 29; Indels
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CA919262.1
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KEYWORDS
SOURCE
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CA919262/c
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                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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llarity 95.1%; Pred. No. 3.1e-78;
Conservative 0; Mismatches 33; Indels 4;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                Score 620.6; DB 12; Length 630;
Pred. No. 4.4e-72;
0; Mismatches 7; Indels 0;
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Plate: 006 row: A column: 08
Seg primer: TCACACAGGAAACAGCTATGAC.
                              Location/Qualifiers
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Best Local Similarity 98.9
Matches 623; Conservative
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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1 (bases 1 to 630)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
                                                                                                                                                                                                                                                                                                                                                           1807
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Medicago truncatula cDNA clone
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                                                            1511
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 AAACGCTTAGGTTCTGGAATGTTTCCCTTCCCTAAATCACAGAATACTGAAAGTGAAA
                                                                                                                                         AAACGCTTAGGTTCTGGAATGTTTTCCCTTCCCCTAAATCACAGAATACTGAAGTGAAA
                                                                                                                                                                                               GGAGAGCCTTGGAGGGAGCTATAAAAGTTTTGATATGGCTGCCGGTGA----TATTCCTG
                                                            GGGTTCTCTATCTTGCCATCTCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATG
                                                                             GGGTTCTCTATCTTGCCATCTCCCGGATGGACAGACTATTGTAACTGGAGCTGGAGATG
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Plant Biology Division
The Samuel Bolosy Division
The Samuel Boberts Noble Foundation
Tel: 580 221 7391
Fax: 580 221 7380
Faxi: 580 221 7380
Faxi: 980 221 7380
Insert Length: 630 5td Error: 0.00
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Spermatophyta; Magnollophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. . . (bases 1 to 1633)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Direct Submission

Submitted (12-APR-2002) Maize Mapping Project, University of

Missouri, Columbia, Mo 65211, USA

If you are interested in getting corresponding physical clones,

If you are publicily available from ZmDs and may be found by BLAST

searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,

www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.
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                                                           181 AGATCTGCTTCGAAATTCGCTTTGTTTGATATCAATACTCCGACGGAAGAAGACGCGATGAT
                                                                                                                                                                                                                                                                                             301 CCGGTTACGCCGGAGAAACCGACTCGCCGTCGATGACATTGCCGAATAGGAATATTTT
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                                                                                                                                                                                                                                                    470 CCGGTTACGCCGGAAAAACCGACTCGCCGTCGATGACATTGCCGAATAGGAATATTTTT
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                         <u> AGATCTGCTTCGAAATTCGCTTTGTTTGATATCAATACTCCGACAGAAGGACGCGATGAT</u>
                                                                                                                                      AGTTCCAGCGCTTATACGACTCTTCTGAGAACGGCGTTGGTTTGGACCGGATGTTGCCCGGT
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Unpublished (2002)
2 (bases 1 to 1633)
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/organism="Medicago truncatula"
/mol_type="mrancatula"
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/db xref="raxon:380"
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids
, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 594)
1 orres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished
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NF069G04FLIF1036 Developing flower Medicago truncatula cDNA clone
NF069G04FL 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: May GD
Plant Biology Division
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7380
Fax: 580 221 7380
Email: 9dmay@noble.org
Insert Length: 594 Std Brror: 0.00
Plate: 069 row: G column: 04
Seg primer: TCACACAGABAACAGTATGAC.
Location/Qualifiers
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Best Local Similarity 98.0%;
Matches 582; Conservative
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HTC 17-0CT-2002

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/lab host="Monte securing, 2 week Old, ellotted / Lab host="Monte securing, 2 week Old, ellotted / Lab host="Monte libe"Gm-c1059"
/clone libe"Gm-c1059"
/clone libe"Gm-c1059"
/clone libe"Gm-c1059"
/mole recomplementary was constructed from mRNA isolated from 2 week old etiolated whole seedlings of P1468916.
Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcorI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcorI. XhoI restriction site of the Bluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa state university."
                                                                                                                            648 bp mRNA linear EST 28-NOV-2001 saa35d02.y1 Gm-c1059 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1059-939 5' similar to TR:Q9XED5 Q9XED5 CELL CYCLE SWITCH BGO44933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, Shoemaker, R., Kelm, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Marran, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Y., Person, B., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae;
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Public. Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further informa
call: (800)-533-4363 or contact via email: cou@resgen.com
High quality sequence stop: 405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mkN4"
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|clone="CENOWS SYSTEMS CLONE ID: Gm-c1059-939"
|/tissue_type="Whole seedling, 2 week old, etiolated"
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Pred. No. 5.2e-62;
0; Mismatches 65; Indels 0;
AGGAACATCTTTCGTTAGAAGCTACATCCGGTGA 1024
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sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis go to
http://www.genome.clemson.edu/projects/peach. To order
this clone go to http://www.genome.clemson.edu/orders
144 c 174 g 187 t 3 others
tissue_type="Mesocarp'
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BU042571.
BU042571.1 GI:22482648
BST.
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1 (bases 1 to 677)
Callahan,A., Palmer,M., Main,D., Wing,R. and Abbott,A.
Peach Model Genome for Rosaceae
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Dept of Genetics and Biochemistry
Clemson University
122 Long Hall, Clemson University, Clemson, SC
Tel: 864 656 3060
Fax: 864 656 6879
Email: aalbertgeclemson.edu
Total High Quality bases = 577
Seg primer: TAATACGACTCACTATAGG
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/organism="Prunus persica"
/mol_type="mRNA"
/culfivar="Loring"
/db_xref="teaxon:3760"
/clone="PP_LEa0013C06f"
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AUTHORS
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COMMENT
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13; Length 677;
Score 499.4; DB 13; Length
Pred. No. 3.1e-56;
0; Mismatches 104; Indels
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Gossyptum arboreum Eukaryothyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids Spermatophyta; Malvaceae; Malvaceae; Gossyptum. 1 (bases 1 to 987)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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tissue_type="Pibers isolated from bolls harvested 7-10
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/note="Vector: pBK-CMV; Site_1: BCoRI; Site_2: XhoI"
203 c 256 g 265 t 5 others
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Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence start: 40
High quality sequence stop: 800.
Location/Qualifiers
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Best Local Similarity 82.2
Matches 550; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/mcl type="mRNA"
/mlltvar=genotype A17"
/dlltvar=genotype A17"
/dlstae_rype="genotype A17"
/dlstae_rounderion with Sinorhizobium meliloti"
/hot="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inculation with Sinorhizobium meliloti. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gagapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: vance004@maroon.tc.umn.edu
University of Minnesota name:M256650e
TIGR sequence name:WTCBR29TK
More information is available at. . http://chrysie.tamu.edu/medicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                      Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
11 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5115
Fax: 651-649-5058
                                                                                                                                                                                                          Fedorova,M., Fierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Pe,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M. ESTS from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1320 AGGTTTGCAATCTTGTCTGGTCCAAAAATGTCAACGAACTAGTAAGCACACATGGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGGTTTGCAATCTTGTCTGGTCCAAAATGTGGAAGAACTAGTAAGCACACATGGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1380 CCCAGAACCAGATTATTGTTTGGAGATACCCCACTATGTCAAAGCTGGCGACTCTTACCG
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                                           Medicago truncatula (barrel medic)
Medicago truncatula
  AW980816.1 GI:8172357
                                                                                                                                                               Medicago.
1 (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                truncatula
Unpublished
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Matches 514;
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CA837263 680 bp mRNA linear BST 12-DEC-2002 MCT003C07_164457 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase IV (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT003C07 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Caprmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Nodule; Vector: pSPORTI; Site 1: SalI; Site 2: NotI; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGAACTGCAGATAGATGTATTCGTTTTTGGAATACAACCACAAACTCACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 AGCTGTAIGGACACTGGAAGTCAGGTAIGCAACCTTGTCTGGTCCAAAAAATGTCAATGAA
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                                                                                                                                                                                                                                                                                                                                  DB 14; Length 528;
1. .528
/organism="Lotus japonicus"
/mol_type="mmNA"
/cultivar="difu" (B-129) "
/db_xref="taxon:34305"
/db_yref="saxon:34305"
/do_regge="5 and 7 week-old plants"
/clone lib="Lotus japonicus nodule library
week-old"
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                                                                                                                                                                                                                                                                                                                                  Score 463.4; DB 14; Length
Pred. No. 1.9e-51;
0; Mismatches 37; Indels
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Best Local Similarity 92.9%;
Matches 485; Conservative
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CB828401
EST.
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Lotus japonicus
Licus japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicctyledons; core eudiccts; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

[ (Dases I to 528)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTE: tools for functional genomics
Unpublished
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        GGGTGAGGGCCTTATCTTGGAGCTCTTCTCTGTTATCTTCTGGTAGTCGTGATAAGAGCA 149
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                                                                                                                                                       210 CAGAGGTTTGTGGGCTGAAGGGTCTTATGACAACCGGGAGCTAGCATCTGGCGGAAATG
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Max Planck Institute of Molecular Plant Physiology
Max Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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High quality sequence stop: 528.
Location/Qualifiers
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OSUNEGLICI8.f OSUNE Oryza sativa (japonica cultivar-group) CDNA clone OSUNEGLICI8 5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzeae; Oryza
1 (bases 1 to 856)
Jantaeuriyaratı, C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,G., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
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                                                                                                                502 ATAGCCTAGCATGTCAAAGTTGGCAACTCTTACAGGACACACTTACAGAGTTCTTTATCT
                                                                      1465 IGCCATCTCCAGATGGACAGACTATTGTAACTGGAGCTGGAGATGAAACGCTTAGGTT
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                                                                                                                                                                                                                                    622 CIGGAATGICTICCCTICTCCCAGICTCAGAACACTGAIAGCGAGCTCGGA 673
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Arizona Genomics Institute
Miroratty of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: C column: 18
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/clone_lib="OSJNEe"
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PCR PRimers
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Best Local Similarity 75.99
Matches 503; Conservative
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/mol_type="mRNA"
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/tlssue_type="leaf"
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/clone_lib="Icc plant Lambda Uni-Zap XR expression library
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/clone_lib="Icc plant Lambda Uni-Zap XR expression library
/clone_lib="Icc plant Lambda Uni-Zap XR lluescript SK-; Site_1:
EcoRI: Site_2: Xhol; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector on cDNA synthesis kit."
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                                          database for the common ice plant,
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Contract: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USP
Tel: 775-784-1918
Fax: 775-784-1650
Email: joushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
BACKWARD: T3 21mer
BACKWARD: T3 21mer
BACKWARD: T3 21mer
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                                          An expressed sequence tag data
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 710)
Alcala,J., Verbalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue
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TAMU Lycopersicon esculentum cDNA clone
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    ATTGGGGAATTGTGTTATTGGAATGCATGCAGCAACAAGGTCACCAAGCTATGTGA
                                                                                                                          retaeegacaaaccaaeegaaaerrcarerareegaaeecacrceareraaeaaaaaaa
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                                                                                                                                                       ATCAATGGAGGGCCATCGGTTACGTGGGGGCCTTGGCCTGGAGTTCATCTTTTGTC
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                                                                                                                                                                                                                                                                                                                                             TITGGGGGTTGATGATTGTGTTGTTCTGTTGGTTGGGCTCAACGTGGTACTCATCTTGC
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEC25N23"
/tissue_type="callus"
/dev_stage="25-40 days old"
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Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
jeurosids I; Fabales; Fabaceae, Papilionoideae, Trifolieae;
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/clone_lib="tomato callus, TAMU"
/note="vector: palueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
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1 (bases 1 to 460)
Pirmaber, C., Bartelsmeier, V., Meyer, F., Bartels, D., Bekel, T.,
Linke, B., Puehler, A. and Kuester, H.
                                                                                                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                                                                                               Query Match
19.5%; Score 392; DB 9; Length 71
Best Local Similarity 79.5%; Pred. No. 3.4e-42;
Matches 464; Conservative 0; Mismatches 120; Indels
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AJ498616 MTPOSE Medicago tz
mRNA sequence.
AJ498616.1 GI:22089059
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/dote="Yeveror: pRluescript II SK+; Water stress was
/dote="Yeveror: pRluescript"
/dote="Yeveror: pRluescript"
/dev stage from control (Well watered) and stressed
/deveror: plants at 2 days before heading, at heading, SO* flowering
/deveror: flowering and 4 days after 50* flowering
/deveror: flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 4 days after 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and 50* flowering and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by S. Rudd of the (http://mips.gsf.de
                         Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Emhartocidaes; Oryzeae; Oryza.
1 (Dases 1 to 909)
Bennett, J., Arumugam, K., Lafitte, R., Wen, J., Rudd, S. and
Enskiewich, R.M.
IRRI Drought Stress Panicle cDNA Library
Orpholished
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    909
        (coganism="Oryza sativa (indica cultivar-group)" (pol.type="mRNA" (cultivar="IR64" (cultivar="IR64")

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +63-2-845-0606
Email: r.bruskiewich@cgiar.org
International Rice Information System (IRIS;
http://www.iris.irri.org): D0200596
Assignment of putative function to the sequence l
Munich Information Center for Protein Sequences
                                                                                                                                                                                                                                                                                                                              replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 342; DB 14;
80.1%; Pred. No. 1e-35;
ative 0; Mismatches 100;
                                                                                                                                                                                                                                                                                                                     On Dec 2, 2002 this sequence version recontact: Richard Bruskiewich
Biometrics and Bioinformatics Unit
International Rice Research Institute
DAPO 7777, Metro Manila, Philippines
Tel: +63-2-845-0563
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Location/Qualifiers
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Best Local Similarity 80.1
Matches 402; Conservative
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                                                                                                                                                                                                                                                                  /organism="Medicago truncatula"
/mol_type="mRXM"
/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="mt--acc95206g07"
/clone="tasue_type="pods including seeds"
/dev_stage="different stages of development"
/clone lib="MTPOSE"
/ fore="Weetor: pGEM-T; Site_1: Pst1; Site_2: Sph1;
/note="Weetor: pGEM-T; Site_1: Pst2; Sph1;
/note="Weetor stages of development. The cDNA was
directionally ligated by Medicenomix into the pGEM-T
vector from Promega using GCATGCGGCCGAGGCCGACATG and
CTGCAGGCCATATGGCCGG adapters. Plasmids containing cDNA
inserts were propagated in E. coli DH10B cells."
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AF53-Rpf 02 I21 T7 085.abl IRRI Drought Stress Paniacle Library toryza sativa (indica cultivar-group) cDNA clone C0000597 5' similar PMCI-TFG2 intergenic region, mRNA sequence.

CA764180.2 GI:27545893
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Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17 Unpublished Contact: Kuester H Lehrstuhl fuer Genetik Universitate Bielefeld Florit Postfach 100131, D-33501 Bielefeld, Germany.
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Pred. No. 4.9e-40;
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Best Local Similarity 91.6%;
Matches 423; Conservative (
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Db 362 ACATTGACGGCCATACATATAGGGTATTATTTAGCCATCCCCAGATGGACT 421

Qy 1490 ATTGTAACTGGAGATGAAACGCTTAGGTTTTGGAATGTTTTCCCTTCCCTAAA 1549

Db 422 ATAGTAACTGGAGATGAAACGCTTCGGTTTTGGAACGTTTCCATCTCCCAAG 481

Qy 1550 TCACAGAATACTGAAAA 1571

Db 482 TCCCAGAGTTCTGAAA 503

Search completed: January 23, 2004, 21:05:55

Job time: 4362 secs
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